

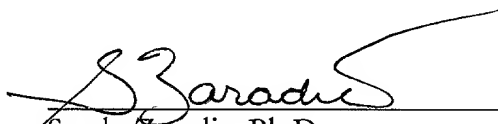
Applicant's Reference: DX01170K US

Title of Invention: MAMMALIAN RECEPTOR PROTEINS;
RELATED REAGENTS AND METHODS

Applicant: Daniel M. Gorman

Sequence Listing Statement

The undersigned agent for applicant hereby declares that the information recorded on the diskette is identical in content to the information in the written Sequence Listing.


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Patent Agent
Registration No. 45,997

Date: May 22, 2001

SEQUENCE SUBMISSION

SEQ ID NO: 1 is primate DCRS6 nucleotide sequence.
 SEQ ID NO: 2 is primate DCRS6 polypeptide sequence.
 SEQ ID NO: 3 is primate DCRS6 reverse translation.
 SEQ ID NO: 4 is rodent DCRS6 nucleotide sequence.
 SEQ ID NO: 5 is rodent DCRS6 polypeptide sequence.
 SEQ ID NO: 6 is rodent DCRS6 reverse translation.
 SEQ ID NO: 7 is primate DCRS7 nucleotide sequence.
 SEQ ID NO: 8 is primate DCRS7 polypeptide sequence.
 SEQ ID NO: 9 is primate DCRS7 reverse translation.
 SEQ ID NO: 10 is rodent DCRS7 nucleotide sequence.
 SEQ ID NO: 11 is rodent DCRS7 polypeptide sequence.
 SEQ ID NO: 12 is rodent DCRS7 reverse translation.
 SEQ ID NO: 13 is primate DCRS8 nucleotide sequence.
 SEQ ID NO: 14 is primate DCRS8 polypeptide sequence.
 SEQ ID NO: 15 is primate DCRS8 reverse translation.
 SEQ ID NO: 16 is primate DCRS9 nucleotide sequence.
 SEQ ID NO: 17 is primate DCRS9 polypeptide sequence.
 SEQ ID NO: 18 is primate DCRS9 reverse translation.
 SEQ ID NO: 19 is rodent DCRS9 nucleotide sequence.
 SEQ ID NO: 20 is rodent DCRS9 polypeptide sequence.
 SEQ ID NO: 21 is rodent DCRS9 reverse translation.
 SEQ ID NO: 22 is primate DCRS10 nucleotide sequence.
 SEQ ID NO: 23 is primate DCRS10 polypeptide sequence.
 SEQ ID NO: 24 is primate DCRS10 reverse translation.
 SEQ ID NO: 25 is rodent DCRS10 nucleotide sequence.
 SEQ ID NO: 26 is rodent DCRS10 polypeptide sequence.
 SEQ ID NO: 27 is rodent DCRS10 reverse translation.
 SEQ ID NO: 28 is primate IL-17 receptor peptide sequence.
 SEQ ID NO: 29 is rodent IL-17 receptor peptide sequence.
 SEQ ID NO: 30 is worm IL-17 receptor peptide sequence.
 SEQ ID NO: 31 is worm DCRS6 nucleotide sequence.

<110> Gorman, Daniel M.

<120> Mammalian Receptor Proteins; Related Reagents and Methods

<130> DX01170K US

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<150> US 60/206,862

<151> 2000-05-24

<160> 31

<170> PatentIn Ver. 2.0

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<223> Description of Unknown Organism:primate; surmised Homo sapiens

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 Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp
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 85 90 95
 acc aga ccc tct ggt ggt aaa tgg aca ttt tcc tat atc ggc ttc cct 384
 Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro
 100 105 110
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 Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn
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 gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat ttc acc tca 480
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 130 135 140 145
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 Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys
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 gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag aag aat gag 576
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 Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr
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Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro	
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gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc	1248
Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro	
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agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc	1296
Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys	
405 410 415	
agt gat cta aga agc cag att cat ctg cac aaa tac gtg gtg gtc tac	1344
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ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt gca gaa ctt      1440
Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu
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ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca caa gcc tgc      1488
Leu His Val Lys Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys
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His Asp Gly Cys Cys Ser Leu
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Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
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Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
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Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
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Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
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 Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
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 Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
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 Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
 245 250 255
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 355 360 365 370
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 375 380 385
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 Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
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 Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
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 Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
 435 440 445 450

05363818 0536301

Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
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056334 052304

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 wsngtntgyc cnaartayca yytnatgaar gaygcnacng cnttytgygc ngarytnytn 1440
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 Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
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 Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
 35 40 45
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 Asp Ser Cys Ser Pro Leu
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atg cct gtg ccc tgg ttc ttg ctg tcc ttg gca ctg ggc cga agc cag 228
Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
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Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
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Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
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His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
45 50 55 60
gac ctc tgt ctg cgt gtg gct gtc cac ttg gcc gtg cat ggg cac tgg 468
Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
65 70 75
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Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
80 85 90
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Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
95 100 105
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Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
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Tyr	Leu	Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu	Trp	Asp	
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Asp	Asp	Leu	Gly	Ala	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile	His	
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Lys	Arg	Trp	Ala	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Phe	Ala	Ala	Ala	
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Leu	Ser	Leu	Ile	Leu	Leu	Leu	Lys	Lys	Asp	His	Ala	Lys	Gly	Trp	Leu	
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Arg	Leu	Leu	Lys	Gln	Asp	Val	Arg	Ser	Gly	Ala	Ala	Ala	Arg	Gly	Arg	
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Ala	Ala	Leu	Leu	Leu	Tyr	Ser	Ala	Asp	Asp	Ser	Gly	Phe	Glu	Arg	Leu	
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Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Cys	Gln	Leu	Pro	Leu	Arg	Val	Ala	
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Trp	Phe	His	Ala	Gln	Arg	Arg	Gln	Thr	Leu	Gln	Glu	Gly	Gly	Val	Val	
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cgc	gcc	tgc	ctc	agc	tgc	gtg	ctg	ccc	gac	ttc	ttg	cag	ggc	cgg	gcg	2004
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Pro	Gly	Ser	Tyr	Val	Gly	Ala	Cys	Phe	Asp	Arg	Leu	Leu	His	Pro	Asp	
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Ala	Val	Pro	Ala	Leu	Phe	Arg	Thr	Val	Pro	Val	Phe	Thr	Leu	Pro	Ser	
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Gln	Leu	Pro	Asp	Phe	Leu	Gly	Ala	Leu	Gln	Gln	Pro	Arg	Ala	Pro	Arg	

Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
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cca gcc ctg gat agc tac ttc cat ccc ccg ggg acn tcc gcg ccg gga 2244
Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Xaa Ser Ala Pro Gly
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Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
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His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
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Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
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Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
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Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
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Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
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Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
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Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
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Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp Ala
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Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val

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Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala 270 275 280		
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Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala 430 435 440		
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Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp
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Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
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Arg Pro Val Pro Asp Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr	
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Phe	Leu	Val	Ala	Val	Ser	Ala	Ile	Ala	Glu	Lys	Leu	Arg	Gln	Ala	Lys
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Gln	Ser	Ser	Ser	Ala	Ala	Leu	Ser	Lys	Phe	Ile	Ala	Val	Tyr	Phe	Asp
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Lys	Gln	Phe	Val	Pro	Phe	His	Pro	Pro	Pro	Leu	Arg	Tyr	Arg	Glu	Pro
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Val	Leu	Glu	Lys	Phe	Asp	Ser	Gly	Leu	Val	Leu	Asn	Asp	Val	Met	Cys
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Lys	Pro	Gly	Pro	Glu	Ser	Asp	Phe	Cys	Leu	Lys	Val	Glu	Ala	Ala	Val
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Gly	Leu	Asp	Gln	Asp	Gly	Glu	Ala	Arg	Pro	Ala	Leu	Asp	Gly	Ser	Ala
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gayaaytgya cnacntayyt naayccngtn ggnaarcayg tnathgnga ygcncaraay 240

athacnathw sncartaygc ntgycaygay cargtngcng tnacnathyt ntggwsnccn 300

ggngcnytn gnathgartt yytnaarggn ttymngtna thytnhgarga rytnaarwsn 360

garggnmgnc arnnncarca rytathytn aargayccna arcarnnnaa ywsnwsntty 420

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ccncayaayt tyggnttymg nttytityay ytncaytaya arytnaarca ygarggnccn 720

ttyaarmgna aracntgyaa rcargarcar acnacngara tgacnwsntg yytnytnar 780

aaygtnwsnc cngngayta yathathgar ytngtngayg ayacnaayac nacnmgnaar 840

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<211> 2012
<212> DNA
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<222> (1)..(1971)

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<221> mat_peptide
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Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro	
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cac tgg aac acc cgc tgt cct ctg gcc tcc cac acg gaa gtt ctg cct	144
His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro	
10 15 20 25	
ata tcc ctt gcc gca cct ggt ggg ccc tct tct cca caa agc ctt ggt	192
Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly	
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Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys	
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cag gtg gct cag gtc ttc aac ggg gcc tct tcc acc tcc tgg tgc aga	288
Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg	
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aat cca aaa agt ctt cca cat tca agt tct ata gga gac aca aga tgc	336
Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys	
75 80 85	
cag cac ctg ctc aga gga agc tgc tgc ctc gtc gtc acc tgt ctg aga	384
Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg	
90 95 100 105	
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Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp	
110 115 120	
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Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val	
125 130 135	
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Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn	
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Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu	
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Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu	
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Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu	
190 195 200	

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gag Glu	ctg Leu	cct Pro 220	tat Tyr	gaa Glu	ttc Phe	ctt Leu	ctg Leu 225	ccc Pro	tgt Cys	ctg Leu	tgc Cys	ata Ile 230	gag Glu	gca Ala	tcc Ser	768
tac Tyr	ctg Leu 235	caa Gln	gag Glu	gac Asp	act Thr	gtg Val 240	agg Arg	cgc Arg	aaa Lys	aaa Lys	tgt Cys 245	ccc Pro	ttc Phe	cag Gln	agc Ser	816
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gac Asp	tac Tyr	agc Ser	cag Gln	cac His 270	act Thr	cag Gln	atg Met	gtc Val	atg Met	gcc Ala	ctg Leu	aca Thr	ctc Leu	cgc Arg 280	tgc Cys	912
cca Pro	ctg Leu	aag Lys	ctg Leu 285	gaa Glu	gct Ala	gcc Ala	ctc Leu	tgc Cys 290	cag Gln	agg Arg	cac His	gac Asp	tgg Trp 295	cat His	acc Thr	960
ctt Leu	tgc Cys	aaa Lys 300	gac Asp	ctc Leu	ccg Pro	aat Asn	gcc Ala 305	acg Thr	gct Ala	cga Arg	gag Glu	tca Ser 310	gat Asp	ggg Gly	tgg Trp	1008
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caa Gln 330	cca Pro	tgg Trp	ttc Phe	tct Ser	ttt Phe 335	gga Gly	aac Asn	agc Ser	agc Ser	cat His 340	gtt Val	gaa Glu	tgc Cys	ccc Pro	cac His 345	1104
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aag Lys 410	cac His	ctc Leu	ttg Leu	tgt Cys	cca Pro 415	gat Asp	gtc Val	tct Ser	tac Tyr	aga Arg 420	cac His	ctg Leu	ggg Gly	ctc Leu	ttg Leu 425	1344
atc Ile	ctg Leu	gca Ala	ctg Leu 430	ctg Leu	gcc Ala	ctc Leu	ctc Leu	acc Thr	cta Leu 435	ctg Leu	ggg Gly	gtt Val	gtt Val	ctg Leu 440	gcc Ala	1392

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Gln	His	Leu	Leu	Arg	Gly	Ser	Cys	Cys	Leu	Val	Val	Thr	Cys	Leu	Arg	
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Leu	Pro	Glu	Ala	Arg	Ala	Ile	Arg	Val	Thr	Ile	Ser	Ser	Gly	Pro	Glu	
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Glu	Leu	Pro	Tyr	Glu	Phe	Leu	Leu	Pro	Cys	Leu	Cys	Ile	Glu	Ala	Ser	
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Tyr	Leu	Gln	Glu	Asp	Thr	Val	Arg	Arg	Lys	Lys	Cys	Pro	Phe	Gln	Ser	
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Pro	Leu	Lys	Leu	Glu	Ala	Ala	Leu	Cys	Gln	Arg	His	Asp	Trp	His	Thr	
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Tyr	Val	Leu	Glu	Lys	Val	Asp	Leu	His	Pro	Gln	Leu	Cys	Phe	Lys	Val
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Lys	His	Leu	Leu	Cys	Pro	Asp	Val	Ser	Tyr	Arg	His	Leu	Gly	Leu	Leu
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<211> 1971
<212> DNA
<213> reverse translation
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Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu
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Ser Leu Pro Leu Leu Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala
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Cys Pro Cys Leu Arg Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg
5 10 15 20

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Val Asp Lys Arg Phe Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu
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gtg agg aaa tct aaa agt cct cct aaa ttt gaa gac tat tgg agg cac 302

09263318 "09263318"

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Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro																
1 5 10 15																
agt cag ttg ctg aaa cca atc cca gaa tat tcc ccg gaa gag gaa tca																275
Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser																
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gaa cca cct gct cca aat ata agg aac atg gca ccc aac agc ttg tct																323
Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser																
35 40 45																
gca ccc aca atg ctt cac aat tcc tcc gga gac ttt tct caa gct cac																371
Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His																
50 55 60																
tca acc ctg aaa ctt gca aat cac cag cgg cct gta tcc cgg cag gtc																419
Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val																
65 70 75 80																

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Arg	Arg	His	Pro	Gly	Leu	Gly	Lys	Ala	Phe	Pro	Ser	Gly	Cys	Ser	Ala	
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Val	Ser	Glu	Pro	Ala	Ser	Glu	Ser	Val	Val	Gly	Ala	Leu	Pro	Ala	Glu	
				115					120				125			
cat	cag	ttt	tca	ttt	atg	gaa	aaa	cgt	aat	caa	tgg	ctg	gta	tct	cag	611
His	Gln	Phe	Ser	Phe	Met	Glu	Lys	Arg	Asn	Gln	Trp	Leu	Val	Ser	Gln	
				130					135				140			
ctt	tca	gcg	gct	tct	cct	gac	act	ggc	cat	gac	tca	gac	aaa	tca	gac	659
Leu	Ser	Ala	Ala	Ser	Pro	Asp	Thr	Gly	His	Asp	Ser	Asp	Lys	Ser	Asp	
				145					150				155			
caa	agt	tta	cct	aat	gcc	tca	gca	gac	tcc	ttg	ggc	ggg	agc	cag	gag	707
Gln	Ser	Leu	Pro	Asn	Ala	Ser	Ala	Asp	Ser	Leu	Gly	Gly	Ser	Gln	Glu	
				165					170				175			
atg	gtg	caa	cgg	ccc	cag	cct	cac	agg	aac	cga	gca	ggc	ctg	gat	ctg	755
Met	Val	Gln	Arg	Pro	Gln	Pro	His	Arg	Asn	Arg	Ala	Gly	Leu	Asp	Leu	
				180					185				190			
cca	acc	ata	gac	acg	gga	tat	gat	tcc	cag	ccc	cag	gat	gtc	ctg	ggc	803
Pro	Thr	Ile	Asp	Thr	Gly	Tyr	Asp	Ser	Gln	Pro	Gln	Asp	Val	Leu	Gly	
				195					200				205			
atc	agg	cag	ctg	gaa	agg	ccc	ctg	ccc	ctc	acc	tcc	gtg	tgt	tac	ccc	851
Ile	Arg	Gln	Leu	Glu	Arg	Pro	Leu	Pro	Leu	Thr	Ser	Val	Cys	Tyr	Pro	
				210					215				220			
cag	gac	ctc	ccc	aga	cct	ctc	agg	tcc	agg	gag	ttc	cct	cag	ttt	gaa	899
Gln	Asp	Leu	Pro	Arg	Pro	Leu	Arg	Ser	Arg	Glu	Phe	Pro	Gln	Phe	Glu	
				225					230				235			
cct	cag	agg	tat	cca	gca	tgt	gca	cag	atg	ctg	cct	ccc	aat	ctt	tcc	947
Pro	Gln	Arg	Tyr	Pro	Ala	Cys	Ala	Gln	Met	Leu	Pro	Pro	Asn	Leu	Ser	
				245					250				255			
cca	cat	gct	cca	tgg	aac	tat	cat	tac	cat	tgt	cct	gga	agt	ccc	gat	995
Pro	His	Ala	Pro	Trp	Asn	Tyr	His	Tyr	His	Cys	Pro	Gly	Ser	Pro	Asp	
				260					265				270			
cac	cag	gtg	cca	tat	ggc	cat	gac	tac	cct	cga	gca	gcc	tac	cag	caa	1043
His	Gln	Val	Pro	Tyr	Gly	His	Asp	Tyr	Pro	Arg	Ala	Ala	Tyr	Gln	Gln	
				275					280				285			
gtg	atc	cag	ccg	gct	ctg	cct	ggg	cag	ccc	ctg	cct	gga	gcc	agt	gtg	1091
Val	Ile	Gln	Pro	Ala	Leu	Pro	Gly	Gln	Pro	Leu	Pro	Gly	Ala	Ser	Val	
				290					295				300			
aga	ggc	ctg	cac	cct	gtg	cag	aag	gtt	atc	ctg	aat	tat	ccc	agc	ccc	1139
Arg	Gly	Leu	His	Pro	Val	Gln	Lys	Val	Ile	Leu	Asn	Tyr	Pro	Ser	Pro	
				305					310				315			
												320				

tgg gac caa gaa gag agg ccc gca cag aga gac tgc tcc ttt ccg ggg	1187
Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly	
325 330 335	
ctt cca agg cac cag gac cag cca cat cac cag cca cct aat aga gct	1235
Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala	
340 345 350	
ggg gct cct ggg gag tcc ttg gag tgc cct gca gag ctg aga cca cag	1283
Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln	
355 360 365	
gtt ccc cag cct ccg tcc cca gct gct gtg cct aga ccc cct agc aac	1331
Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn	
370 375 380	
cct cca gcc aga gga act cta aaa aca agc aat ttg cca gaa gaa ttg	1379
Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu	
385 390 395 400	
cgg aaa gtc ttt atc act tat tcg atg gac aca gct atg gag gtg gtg	1427
Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val	
405 410 415	
aaa ttc gtg aac ttt ttg ttg gta aat ggc ttc caa act gca att gac	1475
Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp	
420 425 430	
ata ttt gag gat aga atc cga ggc att gat atc att aaa tgg atg gag	1523
Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu	
435 440 445	
cgc tac ctt agg gat aag acc gtg atg ata atc gta gca atc agc ccc	1571
Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro	
450 455 460	
aaa tac aaa cag gac gtg gaa ggc gct gag tcg cag ctg gac gag gat	1619
Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp	
465 470 475 480	
gag cat ggc tta cat act aag tac att cat cga atg atg cag att gag	1667
Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu	
485 490 495	
ttc ata aaa caa gga agc atg aat ttc aga ttc atc cct gtg ctc ttc	1715
Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe	
500 505 510	
cca aat gct aag aag gag cat gtg ccc acc tgg ctt cag aac act cat	1763
Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His	
515 520 525	
gtc tac agc tgg ccc aag aat aaa aaa aac atc ctg ctg cgg ctg ctg	1811
Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu	
530 535 540	
aga gag gaa gag tat gtg gct cct cca cgg ggg cct ctg ccc acc ctt	1859
Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu	
545 550 555 560	

cag gtg gtt ccc ttg tgacaccgtt catccccaga tcaactgaggc caggccatgt 1914
 Gln Val Val Pro Leu
 565

ttggggcctt gttctgacag cattctggct gaggctggtc ggtagcactc ctggctgggt 1974
 tttttctgtt cctccccgag aggcctcttg gccccagga aacctgttgt gcagagctct 2034
 tccccggaga cctccacaca ccctggcttt gaagtggagt ctgtgactgc tctgcattct 2094
 ctgcttttaa aaaaaccatt gcaggtgcca gtgtcccata tgttcctcct gacagtttga 2154
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 <212> PRT
 <213> Unknown

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 35 40 45
 Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
 50 55 60
 Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val
 65 70 75 80
 Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys
 85 90 95
 Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala
 100 105 110
 Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu
 115 120 125
 His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln
 130 135 140
 Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp
 145 150 155 160
 Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu
 165 170 175

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Met	Val	Gln	Arg	Pro	Gln	Pro	His	Arg	Asn	Arg	Ala	Gly	Leu	Asp	Leu
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Pro	Thr	Ile	Asp	Thr	Gly	Tyr	Asp	Ser	Gln	Pro	Gln	Asp	Val	Leu	Gly
		195					200					205			
Ile	Arg	Gln	Leu	Glu	Arg	Pro	Leu	Pro	Leu	Thr	Ser	Val	Cys	Tyr	Pro
	210					215					220				
Gln	Asp	Leu	Pro	Arg	Pro	Leu	Arg	Ser	Arg	Glu	Phe	Pro	Gln	Phe	Glu
225					230					235					240
Pro	Gln	Arg	Tyr	Pro	Ala	Cys	Ala	Gln	Met	Leu	Pro	Pro	Asn	Leu	Ser
				245					250					255	
Pro	His	Ala	Pro	Trp	Asn	Tyr	His	Tyr	His	Cys	Pro	Gly	Ser	Pro	Asp
			260					265					270		
His	Gln	Val	Pro	Tyr	Gly	His	Asp	Tyr	Pro	Arg	Ala	Ala	Tyr	Gln	Gln
		275					280					285			
Val	Ile	Gln	Pro	Ala	Leu	Pro	Gly	Gln	Pro	Leu	Pro	Gly	Ala	Ser	Val
	290					295					300				
Arg	Gly	Leu	His	Pro	Val	Gln	Lys	Val	Ile	Leu	Asn	Tyr	Pro	Ser	Pro
305					310					315					320
Trp	Asp	Gln	Glu	Glu	Arg	Pro	Ala	Gln	Arg	Asp	Cys	Ser	Phe	Pro	Gly
				325					330					335	
Leu	Pro	Arg	His	Gln	Asp	Gln	Pro	His	His	Gln	Pro	Pro	Asn	Arg	Ala
			340					345					350		
Gly	Ala	Pro	Gly	Glu	Ser	Leu	Glu	Cys	Pro	Ala	Glu	Leu	Arg	Pro	Gln
		355					360					365			
Val	Pro	Gln	Pro	Pro	Ser	Pro	Ala	Ala	Val	Pro	Arg	Pro	Pro	Ser	Asn
	370					375					380				
Pro	Pro	Ala	Arg	Gly	Thr	Leu	Lys	Thr	Ser	Asn	Leu	Pro	Glu	Glu	Leu
385					390					395					400
Arg	Lys	Val	Phe	Ile	Thr	Tyr	Ser	Met	Asp	Thr	Ala	Met	Glu	Val	Val
				405					410					415	
Lys	Phe	Val	Asn	Phe	Leu	Leu	Val	Asn	Gly	Phe	Gln	Thr	Ala	Ile	Asp
			420					425					430		
Ile	Phe	Glu	Asp	Arg	Ile	Arg	Gly	Ile	Asp	Ile	Ile	Lys	Trp	Met	Glu
		435					440					445			
Arg	Tyr	Leu	Arg	Asp	Lys	Thr	Val	Met	Ile	Ile	Val	Ala	Ile	Ser	Pro
	450					455					460				
Lys	Tyr	Lys	Gln	Asp	Val	Glu	Gly	Ala	Glu	Ser	Gln	Leu	Asp	Glu	Asp
465					470					475					480
Glu	His	Gly	Leu	His	Thr	Lys	Tyr	Ile	His	Arg	Met	Met	Gln	Ile	Glu
				485					490					495	

Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe
 500 505 510
 Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His
 515 520 525
 Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu
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 Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu
 545 550 555 560
 Gln Val Val Pro Leu
 565

<210> 24
 <211> 1695
 <212> DNA
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 <222> (1)..(1695)
 <223> n may be a, c, g, or t

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 aarccnathc cngartayws nccngargar garwsngarc cncngcncnc naayathmgn 120
 aayatggcnc cnaaywsnyt nwsngcncnc acnatgytnc ayaaywsnws nggngaytty 180
 wsnrcargcnc aywsnacnyt naarytngcn aaycaycarm gncngtnws nmgnrcargtn 240
 acntgyytnm gnacncargt nytngargay wsngargayw snttytgymg nmgnrcayccn 300
 ggnytnngna argcnttycc nwsnggntgy wsngcngtnw sngarcncgc nwsngarwsn 360
 gtngtnngng cnytnccngc ngarcaycar ttywsnttya tggaraarmg naaycartgg 420
 ytngtnwsnc arytnwsngc ngcnwsnccn gayacnggnc aygaywsnga yaarwsngay 480
 carwsnytnc cnaaygcnws ngcngaywsn ytngngngnw sncargarat ggtncarmgn 540
 ccncarcnc aymgnaaymg ngcnggnytn gayytnccna cnathgayac nggntaygay 600
 wsnrcarcnc argaygtnyt nggnathmgn carytngarm gncnytncc nytnacnwsn 660
 gtntgytayc cncargayt nccnmgnccn ytnmgnwsnm gngarttycc ncarttygar 720
 ccncarmgnt ayccngcntg ygcncaratg ytnccncna ayytnwsncc ncaygcncnc 780
 tggaaytayc aytaycaytg yccnggnwsn ccngaycayc argtnccnta yggncaygay 840
 tayccnmng cngcntayca rcargtnath carccngcny tncnggnca rccnytnccn 900
 ggngcnwsng tnmnggnytn ncayccngtn caraargtna thytnaayta yccnwsnccn 960

05963318 05963318

tgggaycarg argarmgncc ngencarmgn gaytgywsnt tyccnggnyt nccnmgn cay 1020
 cargaycarc cncaycayca rccnccnaay mgngcnggng cncnggnga rwsnytn gar 1080
 tgyccngcng arytnmgnc ncartnccn carccnccnw snccngcngc ngtnccnmgn 1140
 cccnccwsna ayccnccngc nmngggnaen ytnaaracnw snaayytnc ngargarytn 1200
 mgnaargtnt tyathacnta ywsnatggay acngcnatgg argtngtnaa rttygtnaay 1260
 ttyytnytng tnaayggntt ycaracngcn athgayatht tygargaymg nathmgnggn 1320
 athgayatha thaartggat ggarmgntay ytnmgngaya aracngtnat gathathgtn 1380
 gcnathwsnc cnaartayaa rcargaygtn gargngcng arwsncaryt ngaygargay 1440
 garcayggny tncayacnaa rtayathcay mgnatgatgc arathgartt yathaarc ar 1500
 ggnwsnatga ayttymgntt yathccngtn ytnttyccna aygcnaaraa rgarcaygtn 1560
 ccnactggy tncaraayac ncaygtntay wsntggccna araayaaraa raayathytn 1620
 ytnmgnytny tnmngngarga rgartaygtn gcncnccnm gnggncnnyt nccnacnytn 1680
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<210> 25

<211> 1323

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: rodent; surmised
Mus musculus

<220>

<221> CDS

<222> (1) .. (1026)

<400> 25

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Gln	Asp	Leu	Pro	Gly	Pro	Leu	Arg	Ser	Arg	Glu	Leu	Pro	Pro	Gln	Phe	
1				5				10						15		
gaa	ctt	gag	agg	tat	cca	atg	aac	gcc	cag	ctg	ctg	ccg	ccc	cat	cct	96
Glu	Leu	Glu	Arg	Tyr	Pro	Met	Asn	Ala	Gln	Leu	Leu	Pro	Pro	His	Pro	
			20					25					30			
tcc	cca	cag	gcc	cca	tgg	aac	tgt	cag	tac	tac	tgc	ccc	gga	ggg	ccc	144
Ser	Pro	Gln	Ala	Pro	Trp	Asn	Cys	Gln	Tyr	Tyr	Cys	Pro	Gly	Gly	Pro	
		35				40					45					
tac	cac	cac	cag	gtg	cca	cac	ggc	cat	ggc	tac	cct	cca	gca	gca	gcc	192
Tyr	His	His	Gln	Val	Pro	His	Gly	His	Gly	Tyr	Pro	Pro	Ala	Ala	Ala	
		50				55				60						
tac	cag	caa	gta	ctc	cag	cct	gct	ctg	cct	ggg	cag	gtc	ctt	cct	ggg	240
Tyr	Gln	Gln	Val	Leu	Gln	Pro	Ala	Leu	Pro	Gly	Gln	Val	Leu	Pro	Gly	
65					70					75					80	

gca agg gca aga ggc cca cgc cct gtg cag aag gtc atc ctg aat gac	288
Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp	
85 90 95	
tcc agc ccc caa gac caa gaa gag aga cct gca cag aga gac ttc tct	336
Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser	
100 105 110	
ttc ccg agg ctc ccg agg gac cag ctc tac cgc cca cca tct aat gga	384
Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly	
115 120 125	
gtg gaa gcc cct gag gag tcc ttg gac ctt cct gca gag ctg aga cca	432
Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro	
130 135 140	
cat ggt ccc cag gct cca tcc cta gct gcc gtg cct aga ccc cct agc	480
His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser	
145 150 155 160	
aac ccc tta gcc cga gga act cta aga acc agc aat ttg cca gaa gaa	528
Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu	
165 170 175	
tta cgg aaa gtc ttt atc act tat tct atg gac aca gcc atg gag gtg	576
Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val	
180 185 190	
gtg aaa ttt gtg aac ttt ctg ttg gtg aac ggc ttc caa act gcg att	624
Val Lys Phe Val Asn Phe Leu Val Asn Gly Phe Gln Thr Ala Ile	
195 200 205	
gac ata ttt gag gat aga atc cgg ggt att gat atc att aaa tgg atg	672
Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met	
210 215 220	
gag cgc tat ctt cga gat aag aca gtg atg ata atc gta gca atc agc	720
Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser	
225 230 235 240	
ccc aaa tac aaa cag gat gtg gaa ggc gct gag tcg cag ctg gac gag	768
Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu	
245 250 255	
gac gag cat ggc tta cat act aag tac att cat cgg atg atg cag att	816
Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile	
260 265 270	
gag ttc ata agt cag gga agc atg aac ttc aga ttc atc cct gtg ctc	864
Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu	
275 280 285	
ttc cca aat gcc aag aag gag cat gtg ccg acc tgg ctt cag aac act	912
Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr	
290 295 300	
cat gtt tac agc tgg ccc aag aat aag aaa aac atc ctg ctg cgg ctg	960
His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu	
305 310 315 320	

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ctc agg gag gaa gag tat gtg gct cct ccc cga ggc cct ctg ccc acc 1008
 Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr
 325 330 335

ctt cag gtg gta ccc ttg tgacgatggc cactccagct cagtgccagc 1056
 Leu Gln Val Val Pro Leu
 340

ctgtttctcac agcattcttc tagcggagct ggctgggtggc acccaggccc tggaacacct 1116

cttctacaga gtcctctgtc tcttgagtct gagttgtcct cgctgggctt ccagagcttc 1176

agtgcctgga tgctgcaggt gacagaaaca aacatctatg accacaaaaa ctctcatcac 1236

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tcaaataata aaatgattat tctttgt 1323

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<400> 26

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Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro
 35 40 45

Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala
 50 55 60

Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
 65 70 75 80

Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp
 85 90 95

Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser
 100 105 110

Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly
 115 120 125

Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro
 130 135 140

His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser
 145 150 155 160

Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu
 165 170 175

Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val

0906181806301

180										185					190						
Val	Lys	Phe	Val	Asn	Phe	Leu	Leu	Val	Asn	Gly	Phe	Gln	Thr	Ala	Ile						
		195					200					205									
Asp	Ile	Phe	Glu	Asp	Arg	Ile	Arg	Gly	Ile	Asp	Ile	Ile	Lys	Trp	Met						
		210				215					220										
Glu	Arg	Tyr	Leu	Arg	Asp	Lys	Thr	Val	Met	Ile	Ile	Val	Ala	Ile	Ser						
225					230					235					240						
Pro	Lys	Tyr	Lys	Gln	Asp	Val	Glu	Gly	Ala	Glu	Ser	Gln	Leu	Asp	Glu						
				245					250					255							
Asp	Glu	His	Gly	Leu	His	Thr	Lys	Tyr	Ile	His	Arg	Met	Met	Gln	Ile						
			260					265					270								
Glu	Phe	Ile	Ser	Gln	Gly	Ser	Met	Asn	Phe	Arg	Phe	Ile	Pro	Val	Leu						
		275					280					285									
Phe	Pro	Asn	Ala	Lys	Lys	Glu	His	Val	Pro	Thr	Trp	Leu	Gln	Asn	Thr						
		290				295					300										
His	Val	Tyr	Ser	Trp	Pro	Lys	Asn	Lys	Lys	Asn	Ile	Leu	Leu	Arg	Leu						
305					310					315					320						
Leu	Arg	Glu	Glu	Glu	Tyr	Val	Ala	Pro	Pro	Arg	Gly	Pro	Leu	Pro	Thr						
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Leu	Gln	Val	Val	Pro	Leu																
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<210> 27
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 <212> DNA
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<220>
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 cartaytayt gycngngngg nccntaycay caycargtnc cncayggnga yggntayccn 180
 ccngcngcng cntaycarca rgtnytnear ccngcnytn cnggncargt nytnccnggn 240
 gcnmgngcnm gnggnccnmg nccngtnear aargtnathy tnaaygayws nwsnccncar 300
 gaycargarg armgnccngc ncarmnggay ttywsnttyc cnmgnytncc nmnggaycar 360
 ytntaymgnc cncnwsnaa yggngtngar gcncngarg arwsnytnga yytnccngcn 420
 garytnmgnc cncayggnc ncargcnccn wsnytnngcng cngtnccnmg nccnccnwsn 480

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Pro	Val	Gly	Asp	Leu	Phe	Thr	Ala	Ala	Met	Asn	Met	Ile	Leu	Pro	Asp	
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Phe	Lys	Arg	Pro	Ala	Cys	Phe	Gly	Thr	Tyr	Val	Val	Cys	Tyr	Phe	Ser	
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Lys	Ile	Ile	Ile	Leu	Cys	Ser	Arg	Gly	Thr	Gln	Ala	Lys	Trp	Lys	Ala	
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Lys	Pro	Ala	Gly	Asp	Leu	Phe	Thr	Ala	Ala	Met	Asn	Met	Ile	Leu	Pro	
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Ser	Arg	Tyr	Pro	Leu	Met	Asp	Arg	Phe	Glu	Glu	Val	Tyr	Phe	Arg	Ile	
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Gln	Asp	Leu	Glu	Met	Phe	Glu	Pro	Gly	Arg	Met	His	His	Val	Arg	Glu	
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Val Cys Asp Arg Trp Phe Glu Asp Ser Lys Asn Ala Glu Glu Asn Met
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Phe His Ser Ala Tyr Tyr His Pro Arg Cys Gly Ile Tyr Asp Val Ile
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Asn Asn Phe Phe Pro Cys Thr Asp Pro Arg Leu Ala His Ile Ala Leu
85 90 95

Thr Pro Glu Ala Gln Arg Ser Val Pro Lys Glu Val Glu Tyr Val Leu
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Pro Arg Asp Gln Lys Leu Leu Glu Asp Ala Phe Asp Ile Thr Ile Ala
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Asp Pro Leu Val Ile Asp Ile Pro Ile Glu Asp Val Ala Ile Pro Glu
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Asn Val Pro Ile His His Glu Ser Cys Asp Ser Ile Asp Ser Arg Asn
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Asn Ser Lys Thr His Ser Thr Asp Ser Gly Val Ser Ser Leu Ser Ser
165 170 175

Asn Ser